SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNIT, K+betaM2

<130> D0076 NP

<150> US 60/263,872

<151> 2001-01-24

<150> US 60/269,794

<151> 2001-02-14

<160> 73

<170> PatentIn version 3.0

. . .

<210> 1 <211> 3468

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (515)..(1798)

<400> 1

caagcactgt gctaaagtgt ttttcatatg tcatgaaaag ttgtgccaga aaattatggt 60

120

240

300

360

420

535

ttgaacatgg gcagttttct cctaccgtca gctatatcca caagcatcac atgaagtgga

gatotggcag ototgtgtat ttoagtoaag ttocacaatg aaacotgaca ataatggtaa 180

aaaccaatac ggacatotga gtaactgggg aattggcotg cottgcatgt gagottgatg
gaagattgga tatagacgag ttgattatat tttatgaagt agcagotcac taccatccac

catcoagggt ttaaactact ttttcagcat cacttcacct gtggactctt atacattttg
atttcttggg ggaaaaatac tgggataaga ggaggtcatt ttttaataag ttagcatcct

tttccctttc ttacaagttg atccaaagga taaggctgtg actccattgg attgcacctt 480

taaatcaaaa tagcagcagc agaagaaagg gaca atg gct ctg agt gga aac tgt Met Ala Leu Ser Gly Asn Cys

agt cgt tat tat cct cga gaa caa ggg tcc gca gtt ccc aac tcc ttc 583 Ser Arg Tyr Tyr Pro Arg Glu Gln Gly Ser Ala Val Pro Asn Ser Phe

10 15

cot gag gtg gta gag ctg aat gtc ggg ggt caa gtt tat ttt act cgc 631 Pro Glu Val Val Glu Leu Asn Val Gly Gly Gln Val Tyr Phe Thr Arg 25 30 35

					agc Ser 45											679
					acg Thr											727
					aga Arg											775
					cag Gln											823
					gaa Glu											871
					gat Asp 125											919
					gat Asp											967
					ctc Leu											1015
					tcc Ser											1063
					gtt Val											1111
					ttt Phe 205											1159
					aga Arg											1207
					ttt Phe											1255
					tcg Ser											1303
gat	gac	aag	atc	tgg	tca	agc	tac	act	gaa	tat	gtc	ttc	tac	cgt	gag	1351

Asp	Asp 265	Lys	Ile	Trp	Ser	Ser 270	Tyr	Thr	Glu	Tyr	Val 275	Phe	Tyr	Arg	Glu	
														aat Asn		1399
														ctc Leu 310		1447
														gag Glu		1495
gtc Val	atc Ile	tgt Cys 330	ggt Gly	ccc Pro	gtg Val	aca Thr	cgc Arg 335	cag Gln	acc Thr	aac Asn	atc Ile	cag Gln 340	act Thr	ctg Leu	gac Asp	1543
cgt Arg	ccc Pro 345	atc Ile	aag Lys	aag Lys	ggc Gly	cct Pro 350	gtc Val	cag Gln	ctg Leu	atc Ile	caa Gln 355	cag Gln	tca Ser	gag Glu	atg Met	1591
														agg Arg		1639
														tca Ser 390		1687
														aaa Lys		1735
														ctt Leu		1783
	aag Lys 425				taa	ggga	ggg (ctgg	gggc	gg gg	gaaa	aaaa	a aa	aaaa	gagt	1838
cat	ttga	aaa t	ttaad	cctca	at a	aaag	gaati	t car	att	ttaa	agg	aaaa	aaa ·	taca	actaat	1898
gat	gcaca	att 1	tctta	agaa	ca ca	aata	gtcca	a tt	gata	tact	act	gcct	act '	ttac	ctagtt	1958
cac	cttaa	aca 1	tgta	aatc	ca ca	agggi	tagai	t tt	cttt	ctag	atg	tgga	agt a	acaa	gaaaat	2018
ctt	tttta	agt 1	tatti	gtti	tg ti	ttact	ttegi	t cc	catg	tgct	aact	tato	tta ·	tata	taatga	2078
gag	ccago	cta d	cgtaa	aaagt	ta go	ctga	gagge	c ct	tggg	agtc	att	tatc	cca a	aact	gggttt	2138
ttt	etete	cat o	cette	ctaco	et c	cctc	cttt	g aa	tgag	ggta	tgg.	taga	aaa a	agat	etggee	2198
caa	tggca	ata a	agtti	ggaa	at t	ttta	attti	t gg	tttt	tect	ttt	gttt	atg (gggt	ggggg	2258

gaatggcaga	tttatatgac	ttttcactca	aatctatatg	tgccagttta	tattgactcc	2318
gtatgcatga	gtatttgtgc	aacacaagca	caactaagta	tgtatataca	catgacgcac	2378
acgatgccag	ggcctagacc	teccaaggge	tgtgctcctg	ctcccagcag	ccctctctta	2438
gaatatttca	gatggatgag	cttctgactc	tttcttaaaa	ttcttttggg	aagatttccc	2498
agcetttett	cacaacactt	tctaacatca	aatgactctc	atcatcaaca	aattgtattc	2558
cttattgtga	aattaatacc	ctcaggctcc	attttactgc	tttgctcttt	gtctgcatta	2618
agagaggatg	aggagagctg	gtcaaacatt	ccttgtgtta	aaaaaatcaa	acattcatat	2678
ccacaaaatt	ttctgctaaa	tgactccaca	ctcagccttc	tctaccctga	actgaattat	2738
caccctttc	tccatgtttt	cagagttctt	actgcccaca	gtttaatggt	gtggcctttc	2798
cacataatcc	acattaagtt	ctgtgttcct	gtgttgttgt	ggaactaagg	acaacacaca	2858
gtacttgaat	aagggteegg	ccttttgttt	gttttagaga	aagttgtatt	ccacacacaa	2918
cctaataatt	tcttataaaa	attttaaact	acaaagetae	atttttactt	gettgtagee	2978
gtttttgttt	gcctttggga	ttegggettt	ggctgtgccc	atgctaggat	ttagctgtgt	3038
catttttatg	atgtctgtaa	caacccaaca	aggtaactga	ageteeagag	ttaaggtttc	3098
agatttctaa	atgaaactat	ctttttcaat	tacatcctga	cttgtataga	cacagccaaa	3158
aagaaactgt	taatagccat	ccgtccatgt	aactctgtat	tttactaagg	taccaatagc	3218
tetttcatag	acttgtgcta	caagaaggtt	aaaagaccag	ttttattttc	agcattecte	3278
atgcatttca	gtggtaacca	aaaaataatt	tgtcaattaa	tagttgtgtg	ccaagcactc	3338
ctaatttgtt	ttattgcgtg	tgtgtgcatg	tgtgtatgtg	tatcacaggt	aataaaggca	3398
attggatgat	taaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	3458
aaaaaaaaa						3468

Met Ala Leu Ser Gly Asn Cys Ser Arg Tyr Tyr Pro Arg Glu Gln Gly 1 1

Ser Ala Val Pro Asn Ser Phe Pro Glu Val Val Glu Leu Asn Val Gly

<210> 2 <211> 428 <212> PRT <213> Homo sapiens

<400> 2

Gly Gln Val Tyr Phe Thr Arg His Ser Thr Leu Ile Ser Ile Pro His $35 \hspace{1cm} 40 \hspace{1cm} 45$

Ser Leu Leu Trp Lys Met Phe Ser Pro Lys Arg Asp Thr Ala Asn Asp 50 60

Leu Ala Lys Asp Ser Lys Gly Arg Phe Phe Ile Asp Arg Asp Gly Phe 65 70 70 75 75

Leu Phe Arg Tyr Ile Leu Asp Tyr Leu Arg Asp Arg Gln Val Val Leu 85 90 95

Pro Asp His Phe Pro Glu Lys Gly Arg Leu Lys Arg Glu Ala Glu Tyr 100 \$100\$

Phe Gln Leu Pro Asp Leu Val Lys Leu Leu Thr Pro Asp Glu Ile Lys $115 \\ 120 \\ 125$

Gln Ser Pro Asp Glu Phe Cys His Ser Asp Phe Glu Asp Ala Ser Gln 130 135 140

Gly Ser Asp Thr Arg Ile Cys Pro Pro Ser Ser Leu Leu Pro Ala Asp 145 150 155 160

Arg Lys Trp Gly Phe Ile Thr Val Gly Tyr Arg Gly Ser Cys Thr Leu 165 \$170\$

Gly Arg Glu Gly Gln Ala Asp Ala Lys Phe Arg Arg Val Pro Arg Ile 180 $$185\$

Leu Val Cys Gly Arg Ile Ser Leu Ala Lys Glu Val Phe Gly Glu Thr 195 200 205

Leu Asn Glu Ser Arg Asp Pro Asp Arg Ala Pro Glu Arg Tyr Thr Ser 210 215 220

Arg Phe Tyr Leu Lys Phe Lys His Leu Glu Arg Ala Phe Asp Met Leu 225 230 230

Ser Glu Cys Gly Phe His Met Val Ala Cys Asn Ser Ser Val Thr Ala 245 250 255

Ser	Phe	Ile	Asn 260	Gln	Tyr	Thr	Asp	Asp 265	Lys	Ile	Trp	Ser	Ser 270	Tyr	Thr	
Glu	Tyr	Val 275	Phe	Tyr	Arg	Glu	Pro 280	Ser	Arg	Trp	Ser	Pro 285	Ser	His	Cys	
Asp	Cys 290	Cys	Cys	Lys	Asn	Gly 295	Lys	Gly	Asp	Lys	Glu 300	Gly	Glu	Ser	Gly	
Thr 305	Ser	Cys	Asn	Asp	Leu 310	Ser	Thr	Ser	Ser	Cys 315	Asp	Ser	Gln	Ser	Glu 320	
Ala	Ser	Ser	Pro	Gln 325	Glu	Thr	Val	Ile	Cys 330	Gly	Pro	Val	Thr	Arg 335	Gln	
Thr	Asn	Ile	Gln 340	Thr	Leu	Asp	Arg	Pro 345	Ile	Lys	Lys	Gly	Pro 350	Val	Gln	
Leu	Ile	Gln 355	Gln	Ser	Glu	Met	Arg 360	Arg	Lys	Ser	Asp	Leu 365	Leu	Arg	Ile	
Leu	Thr 370		Gly	Ser	Arg	Glu 375	Ser	Asn	Met	Ser	Ser 380	Lys	Lys	Lys	Ala	
Val 385		Glu	Lys	Leu	Ser 390	Ile	Glu	Glu	Glu	Leu 395	Glu	Lys	Суз	Ile	Gln 400	
Asp	Phe	Leu	Lys	Lys 405		Ile	Pro	Asp	Arg 410		Pro	Glu	Arg	Lys 415	His	
Pro	Trp	Gln	Ser 420		Leu	Leu	Arg	Lys 425	Tyr	His	Leu					
<21 <21 <21 <21	1> 2>	3 769 DNA Homo	sap	iens												
<40		3	L L	t o o	a.a	~~~+	aat t	+ +-	a a t +	t at t	200	20++	ant.	0032	aggata	60
-				-		-									aggaca aaggga	120
															cagttc	180
							-			-					ctcgcc	240
cca	actc	ULL	CCCT	yayg	uy g	caya	yerg	a al	yuug	9999	LUd	uyet	Lat	ccca	couget	~ = 0

attoca	catt	gata	agca	tc c	ctca	ttcc	c to	ctgt	ggaa	aat	gttt	tcc	ccaa	agagag	9	300
acacgg	ctaa	tgat	ctag	сс а	agga	ctcc	a ag	ggaa	ggtt	ttt	catt	gac	agag	atggaf	t	360
tcttgt	tccg	ttat	attc	tg g	acta	tctc	a gg	gaca	ggca	ggt	ggtc	ctg	cctg	atcact	t	420
ttccag	aaaa	agga	agac	tg a	aaag	ggaa	g ct	gaat	actt	cca	gctc	cca	gact	tggtca	а	480
aactcc	tgac	cccc	gatg	aa a	tcaa	gcaa	a gc	ccag	atga	att	ctgc	cac	agtg	acttt	3	540
aagatg	cctc	ccaa	ggaa	gc g	acac	aaga	a tc	tgcc	cccc	ttc	ctcc	ctg	ctcc	ctgcc	3	600
accgca	agtg	gggt	ttca	tt a	ctgt	gggt	t ac	agag	gatc	ctg	cacc	ttg	ggca	gagag	9	660
gacagg	caga	tgcc	aagt	tt c	ggag	agtt	c cc	cgga	tttt	ggt	ttgt	gga	agga	tttcct		720
tggcaa	aaga	agtc	tttg	ga g	aaac	tttg	a at	gaaa	gcag	aga	ccct	ga				769
<210> <211> <212> <212> <213>	4 237 PRT Homo	sap	iens													
Met As 1	p Asr	Gly	Asp 5	Trp	Gly	Tyr	Met	Met 10	Thr	Asp	Pro	Val	Thr 15	Leu		
Asn Va	l Gly	Gly 20	His	Leu	Tyr	Thr	Thr 25	Ser	Leu	Thr	Thr	Leu 30	Thr	Arg		
Tyr Pr	o Asp 35	Ser	Met	Leu	Gly	Ala 40	Met	Phe	Gly	Gly	Asp 45	Phe	Pro	Thr		
Ala Ar 50	g Asp	Pro	Gln	Gly	Asn 55	Tyr	Phe	Ile	Asp	Arg 60	Asp	Gly	Pro	Leu		
Phe Ar 65	g Tyr	Val	Leu	Asn 70	Phe	Leu	Arg	Thr	Ser 75	Glu	Leu	Thr	Leu	Pro 80		
Leu As	p Phe	Lys	Glu 85	Phe	Asp	Leu	Leu	Arg 90	Lys	Glu	Ala	Asp	Phe 95	Tyr		
Gln Il	e Glu	Pro 100	Leu	Ile	G1n	Cys	Leu 105	Asn	Asp	Pro	Lys	Pro 110	Leu	Tyr		
Pro Met	t Asp 115		Phe	Glu	Glu	Val 120	Val	Glu	Leu	Ser	Ser 125	Thr	Arg	Lys		
Leu Sei 130		Tyr	Ser	Asn	Pro 135	Val	Ala	Val	Ile	Ile 140	Thr	Gln	Leu	Thr		

Ile Thr Thr Lys Val His Ser Leu Leu Glu Gly Ile Ser Asn Tyr Phe 145 \$150\$

Thr Lys Trp Asn Lys His Met Met Asp Thr Arg Asp Cys Gln Val Ser

Phe Thr Phe Gly Pro Cys Asp Tyr His Gln Glu Val Ser Leu Arg Val

His Leu Met Glu Tyr Ile Thr Lys Gln Gly Phe Thr Ile Arg Asn Thr

Arg Val His His Met Ser Glu Arg Ala Asn Glu Asn Thr Val Glu His 210

Asn Trp Thr Phe Cys Arg Leu Ala Arg Lys Thr Asp Asp

<210> 5 <211> 228

<212> PRT

<213> Drosophila melanogaster

<400> 5

Met Pro Glu Ile Ile Glu Leu Asn Val Gly Gly Val Ser Tyr Thr Thr

Thr Leu Ala Thr Leu Leu Gln Asp Lys Ser Thr Leu Leu Ala Glu Leu

Phe Gly Glu Gly Arg Asp Ser Leu Ala Lys Asp Ser Lys Gly Arg Tyr

Phe Leu Asp Arg Asp Gly Val Leu Phe Arg Tyr Ile Leu Asp Phe Leu

Arg Asp Lys Ala Leu His Leu Pro Glu Gly Phe Arg Glu Arg Gln Arg

Leu Leu Arg Glu Ala Glu His Phe Lys Leu Thr Ala Met Leu Glu Cys

Ile Arg Ser Glu Arg Asp Ala Arg Pro Pro Gly Cys Ile Thr Ile Gly

Tyr Arg Gly Ser Phe Gln Phe Gly Lys Asp Gly Leu Ala Asp Val Lys

Phe Arg Lys Leu Ser Arg Ile Leu Val Cys Gly Arg Val Ala Gln Cys 135

Arg Glu Val Phe Gly Asp Thr Leu Asn Glu Ser Arg Asp Pro Asp His 145

Gly Gly Thr Asp Arg Tyr Thr Ser Arg Phe Phe Leu Lys His Cys Tyr 170

Ile Glu Gln Ala Phe Asp Asn Leu His Asp His Gly Tyr Arg Met Ala 180 185

Gly Ser Cys Gly Ser Gly Thr Ala Gly Ser Ala Ala Glu Pro Lys Pro 195 200 205

Gly Val Asp Thr Glu Glu Asn Arg Trp Asn His Tyr Asn Glu Phe Val

Phe Ile Arg Asp

<210> 6 <211> 190

<212> PRT

<213> Caenorhabditis elegans

<400> 6

Met Thr Ser Val Glu Asp Val Ile Thr Leu Asn Val Gly Gly Thr Met 1 $$ 5 $$ 10 $$ 15

Tyr Thr Thr Thr Arg Ser Thr Leu Ser Lys Glu Thr Asp Thr Leu Leu 20 25 30

Ala Asn Ile Ala Ser Gly Ser Leu Ser Glu Asp Glu Gln Ala Asn Val $35 \hspace{1cm} 40 \hspace{1cm} 45$

Val Thr Leu Pro Asp Gly Thr Leu Phe Val Asp Arg Asp Gly Pro Leu 50 60

Phe Ala Tyr Val Leu His Phe Leu Arg Thr Asp Lys Leu Ser Leu Pro 65 70 75 80

Glu Gln Fhe Arg Glu Val Ala Arg Leu Lys Asp Glu Ala Asp Phe Tyr 85 90 95

Arg Leu Glu Arg Phe Ser Thr Leu Leu Ser Asn Ala Ser Ser Ile Ser 100 105 110

Pro Arg Pro Arg Thr Ala Asn Gly Tyr Asn Thr Ile Thr Ser Gly Ala $115 \\ 120 \\ 125$

Glu Thr Gly Gly Tyr Ile Thr Leu Gly Tyr Arg Gly Thr Phe Ala Phe 130 135 140

Gly Arg Asp Gly Gln Ala Asp Val Lys Phe Arg Lys Leu His Arg Ile 145 \$150\$

Leu Val Cys Gly Arg Ala Thr Leu Cys Arg Glu Val Phe Ala Asp Thr 165 170 175

Leu Asn Glu Ser Arg Asp Pro Gly Gly Pro Asp Asp Gly Glu 180 185 190

<210> 7

<211> 256

<212> PRT

<213> Homo sapiens

```
<220>
<221> variant
<222> (15)..(15)
```

<223> wherein "Xaa" is unknown.

<400> 7

Met Ser Arg Pro Leu Ile Thr Arg Ser Pro Ala Ser Pro Leu Xaa Asn 1 $$ 5 $$ 10 $$ 15

Gln Gly Ile Pro Thr Pro Ala Gln Leu Thr Lys Ser Asn Ala Pro Val 20 25 30

His Ile Asp Val Gly Gly His Met Tyr Thr Ser Ser Leu Ala Thr Leu 35 40 45

Thr Lys Tyr Pro Glu Ser Arg Ile Gly Arg Leu Phe Asp Gly Thr Glu 50 55 60

Pro Ile Val Leu Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp 65 70 75 80

Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser Lys Leu 85 90 95 Leu Ile Pro Asp Asp Phe Lys Asp Tyr Thr Leu Leu Tyr Glu Glu Ala

100 105 110 Lys Tyr Phe Gln Leu Gln Pro Met Leu Leu Glu Met Glu Arg Trp Lys 115 120 125

Gln Asp Arg Glu Thr Gly Arg Phe Ser Arg Pro Cys Glu Cys Leu Val

Val Arg Val Ala Pro Asp Leu Gly Glu Arg Ile Thr Leu Ser Gly Asp 145 150 155

Lys Ser Leu Ile Glu Glu Val Phe Pro Glu Ile Gly Asp Val Met Cys

Asn Ser Val Asn Ala Gly Trp Asn His Asp Ser Thr His Val Ile Arg 180 185 190

Phe Pro Leu Asn Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu 195 200 205

Arg Leu Gln Gln Arg Gly Phe Glu Ile Val Gly Ser Cys Gly Gly Gly 210 215 220

Val Asp Ser Ser Gln Phe Ser Glu Tyr Val Leu Arg Arg Glu Leu Arg 225 230 240

<213> Homo sapiens

```
<210> 8
<211> 80
<212> DNA
<213> Artificial
<220>
<223> Synthetic Oligonucleotide Modified To Contain Biotin at the 5 Pr
       ime En
<400> 8
tgggagctgg aagtattcag cttccctttt cagtcttcct ttttctggaa agtgatcagg
                                                                       60
caggaccacc tgcctgtccc
                                                                       80
<210> 9
<211> 20
<212> DNA
<213> Homo sapiens
<400> 9
tactcgccat tccacattga
                                                                       20
<210> 10
<211> 20
<212> DNA
<213> Homo sapiens
<400> 10
attcatctgg gctttgcttg
                                                                       20
<210> 11
<211> 14
<212> PRT
<213> Homo sapiens
<400> 11
Met Ala Leu Ser Gly Asn Cys Ser Arg Tyr Tyr Pro Arg Glu
<210> 12
<211> 14
<212> PRT
<213> Homo sapiens
<400> 12
Phe Gly Glu Thr Leu Asn Glu Ser Arg Asp Pro Asp Arg Ala
<210> 13
<211> 14
<212> PRT
```

```
<400> 13
His Met Val Ala Cys Asn Ser Ser Val Thr Ala Ser Phe Ile
<210> 14
<211> 14
<212> PRT
<213> Homo sapiens
<400> 14
Gly Ser Arg Glu Ser Asn Met Ser Ser Lys Lys Lys Ala Val
                                      1.0
<210> 15
<211> 13
<212> PRT
<213> Homo sapiens
<400> 15
Leu Trp Lys Met Phe Ser Pro Lys Arg Asp Thr Ala Asn
<210> 16
<211> 13
<212> PRT
<213> Homo sapiens
<400> 16
Ala Pro Glu Arg Tyr Thr Ser Arg Phe Tyr Leu Lys Phe
<210> 17
<211> 13
<212> PRT
<213> Homo sapiens
<400> 17
Arg Glu Ser Asn Met Ser Ser Lys Lys Lys Ala Val Lys
<210> 18
<211> 13
<212> PRT
<213> Homo sapiens
<400> 18
Glu Ser Asn Met Ser Ser Lys Lys Lys Ala Val Lys Glu
                .5
<210> 19
```

```
<211> 18
 <212> PRT
 <213> Homo sapiens
<400> 19
 Phe Pro Glu Lys Gly Arg Leu Lys Arg Glu Ala Glu Tyr Phe Gln Leu
Pro Asp
<210> 20
<211> 103
<212> PRT
<213> Homo sapiens
<400> 20
Glu Val Val Glu Leu Asn Val Gly Gly Gln Val Tyr Phe Thr Arg His
Ser Thr Leu Ile Ser Ile Pro His Ser Leu Leu Trp Lys Met Phe Ser
Pro Lys Arg Asp Thr Ala Asn Asp Leu Ala Lys Asp Ser Lys Gly Arg
Phe Phe Ile Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr
Leu Arg Asp Arg Gln Val Val Leu Pro Asp His Phe Pro Glu Lys Gly
                   70
Arg Leu Lys Arg Glu Ala Glu Tyr Phe Gln Leu Pro Asp Leu Val Lys
Leu Leu Thr Pro Asp Glu Ile
           100
<210> 21
<211> 21
<212> PRT
<213> Homo sapiens
<400> 21
Cys Gly Phe His Met Val Ala Cys Asn Ser Ser Val Thr Ala Ser Phe
Ile Asn Gln Tyr Thr
<210> 22
<211> 17
<212> DNA
<213> Homo sapiens
```

<400> 22 tgggattcgg	gctttgg					17
<210> 23 <211> 26 <212> DNA <213> Hom	o sapiens					
<400> 23 tgttgggttg	ttacagacat	cataaa				26
<210> 24 <211> 29 <212> DNA <213> Hom	o sapiens					
<400> 24 tgacacaget	aaatcctagc	atgggcaca				29
<210> 25 <211> 733 <212> DNA <213> hom						
<400> 25 gggatccgga	gcccaaatct	tctgacaaaa	ctcacacatg	cccaccgtgc	ccagcacetg	60
aattcgaggg	tgcaccgtca	gtcttcctct	tccccccaaa	acccaaggac	accctcatga	120
tctcccggac	teetgaggte	acatgcgtgg	tggtggacgt	aagccacgaa	gaccctgagg	180
tcaagttcaa	ctggtacgtg	gacggcgtgg	aggtgcataa	tgccaagaca	aagccgcggg	240
aggagcagta	caacagcacg	taccgtgtgg	tcagcgtcct	caccgtcctg	caccaggact	300
ggctgaatgg	caaggagtac	aagtgcaagg	tctccaacaa	agccctccca	acccccatcg	360
agaaaaccat	ctccaaagcc	aaagggcagc	cccgagaacc	acaggtgtac	accetgeece	420
catcccggga	tgagctgacc	aagaaccagg	tcagcctgac	ctgcctggtc	aaaggettet	480
atccaagcga	catcgccgtg	gagtgggaga	gcaatgggca	gccggagaac	aactacaaga	540
ccacgcctcc	cgtgctggac	teegaegget	ccttcttcct	ctacagcaag	ctcaccgtgg	600
acaagagcag	gtggcagcag	gggaacgtct	tctcatgctc	cgtgatgcat	gaggetetge	660
acaaccacta	cacgcagaag	agcctctccc	tgtctccggg	taaatgagtg	cgacggccgc	720
gactctagag	gat					733

<210> 26

<212> DNA

```
<211> 8
<212> PRT
<213> bacteriophage T7
<400> 26
Asp Tyr Lys Asp Asp Asp Lys
<210> 27
<211> 39
<212> DNA
<213> Homo sapiens
<400> 27
gcagcagcgg ccgccctgag gtggtagagc tgaatgtcg
                                                                    39
<210> 28
<211> 36
<212> DNA
<213> Homo sapiens
<400> 28
gcagcagtcg actagatgat acttecttaa aagtte
                                                                    36
<210> 29
<211> 39
<212> DNA
<213> Homo sapiens
<400> 29
gcagcagcgg ccgcatggct ctgagtggaa actgtagtc
                                                                    39
<210> 30
<211> 37
<212> DNA
<213> Homo sapiens
<400> 30
gcagcagtcg actgtatatt ggttgatgaa agatgct
                                                                    37
<210> 31
<211> 23
<212> DNA
<213> Homo sapiens
<400> 31
caggtgcage tggtgcagte tgg
                                                                    23
<210> 32
<211> 23
```

tgaagagacg gtgaccattg toco	24
<210> 39	
<211> 24	
<212> DNA	
<213> Homo sapiens	
<400> 39	
tgaggagacg gtgaccaggg ttcc	24
<210> 40	
<211> 24 .	
<212> DNA	
<213> Homo sapiens	
<400> 40	
tgaggagacg gtgaccgtgg tccc	24
5 55 5 15 5.5 5.5 5.5 5.5 5.5 5.5 5.5 5.	2.3
<210> 41	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 41	
gacatccaga tgacccagtc tcc	23
<210> 42	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 42	
gatgttgtga tgactcagtc tcc	23
<210> 43	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 43	
gatattgtga tgactcagtc tcc	23
<210> 44	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 44	
gaaattgtgt tgacgcagtc tcc	23

<210> <211> <212> <213>	23 DNA	
<400> gacat	45 cgtga tgacccagte tec	23
<210> <211> <212> <213>	23 DNA	
<400> gaaac	46 gacac toacgoagto too	23
<210> <211> <212> <213>	23 DNA	
<400> gaaatt	47 ggtgc tgactcagtc tcc	23
<210> <211> <212> <213>	48 23 DNA HOmo sapiens	
<400> cagtct	48 gtgt tgacgcagcc gcc	23
<210> <211> <212> <213>	49 23 DNA Homo sapiens	
<400>	49 gccc tgactcagcc tgc	23
<210> <211> <212>	50 23 DNA	
<213> <400> tcctat	Homo sapiens 50 gtgc tgactcagcc acc	23
<210> <211> <212>	51 23 DNA	

<211> 24 <212> DNA <213> Homo sapiens <400> 57

<213> Homo sapiens <400> 51

23
23
23
23
24
24

acgtttgata tecaetttgg teee	24
<210> 58 <211> 24 <212> DNA <213> Homo sapiens	
<400> 58 acgtttgatc tocaccttgg tecc	24
<210> 59 <211> 24 <212> DNA <213> Homo sapiens	
<400> 59 acgtttaatc tocagtogtg tocc	
augustance socialised section	24
<210> 60 <211> 23 <212> DNA <213> Homo sapiens	
<400> 60	
cagtotgtgt tgacgcagcc gcc	23
<210> 61 <211> 23 <212> DNA <213> Homo sapiens	
<400> 61 cagtetgeec tgaetcagec tge	23
<210> 62 <211> 23 <212> DNA <213> Homo sapiens	
<400> 62 tcctatgtgc tgactcagcc acc	23
<210> 63 <211> 23 <212> DNA <213> Homo sapiens	
<400> 63 tettetgage tgaeteagga ece	23

<21 <21 <21 <21	.1>	64 23 DNA Homo	sap	oiens	3											
<40 cac		64 itac	tgac	tcaa	icc č	icc										23
<21 <21 <21 <21	1> 2>	65 23 DNA Homo	sap	iens												
<40 cag		65 rtge	tcac	tcag	rce g	te										23
<21 <21 <21 <21	1> 2>	66 23 DNA Homo	sap	iens												
<40 aat		66 tgc	tgac	tcag	cc c	ca										23
<21 <21 <21 <21	1> 2> 3>	67 301 PRT Dros	ophi	la m	elan	ogas	ter									
<40		67														
Met 1	Ser	Glu	Ser	Met 5	Ser	Gly	Asp	His	Lys 10	Ile	Leu	Leu	Lys	Gly 15	His	
Ser	Ser	Gln	Tyr 20	Leu	Lys	Leu	Asn	Val 25	Gly	Gly	His	Leu	Tyr 30	Tyr	Thr	
Thr	Ile	Gly 35	Thr	Leu	Thr	Lys	Asn 40	Asn	Asp	Thr	Met	Leu 45	Ser	Ala	Met	
Phe	Ser 50	Gly	Arg	Met	Glu	Val 55	Leu	Thr	Asp	Ser	Glu 60	Gly	Trp	Ile	Leu	
Ile 65	Asp	Arg	Суз	Gly	Asn 70	His	Phe	Gly	Ile	Ile 75	Leu	Asn	Tyr	Leu	Arg 80	
Asp	Gly	Thr	Val	Pro 85	Leu	Pro	Glu	Thr	Asn 90	Lys	Glu	Ile	Ala	Glu 95	Leu	
Leu	Ala	Glu	Ala 100	Lys	Tyr	Tyr	Cys	Ile 105	Thr	Glu	Leu	Ala	Ile 110	Ser	Суз	
Glu	Arg	Ala 115	Leu	Tyr	Ala	His	Gln 120	Glu	Pro	Lys	Pro	Ile 125	Cys	Arg	Ile	

Pro	Leu 130	Ile	Thr	Ser	Gln	Lys 135	Glu	Glu	Gln	Leu	Leu 140	Leu	Ser	Val	Ser	
Leu 145	Lys	Pro	Ala	Val	Ile 150	Leu	Val	Val	Gln	Arg 155	Gln	Asn	Asn	Lys	Tyr 160	
Ser	Tyr	Thr	Ser	Thr 165	Ser	Asp	Asp	Asn	Leu 170	Leu	Lys	Asn	Ile	Glu 175	Leu	
Phe	Asp	Lys	Leu 180	Ser	Leu	Arg	Phe	Asn 185	Glu	Arg	Ile	Leu	Phe 190	Ile	Lys	
Asp	Val	Ile 195	Gly	Pro	Ser	Glu	Ile 200	Cys	Cys	Trp	Ser	Phe 205	Tyr	Gly	His	
Gly	Lys 210	Lys	Val	Ala	Glu	Val 215	Cys	Cys	Thr	Ser	11e 220	Val	Tyr	Ala	Thr	
Asp 225	Arg	Lys	His	Thr	Lys 230	Val	Glu	Phe	Pro	G1u 235	Ala	Arg	Ile	Tyr	G1u 240	
Glu	Thr	Leu	Gln	Val 245	Leu	Leu	Tyr	Glu	Asn 250	Arg	Asn	Ala	Pro	Asp 255	Gln	
Glu	Leu	Met	Gln 260	Ala	Thr	Ser	Ser	Ala 265	Arg	Val	Gly	Ser	Ala 270	Ser	Gly	
Thr	Ser	Ile 275	Asn	Gln	Tyr	Thr	Ser 280	Asp	Glu	Glu	Glu	Glu 285	Arg	Thr	Gly	
Leu	Ala 290	Arg	Leu	Arg	Ser	Asn 295	Lys	Arg	Asn	Asn	Pro 300	Ser				
<210		8														
<211 <212		0 NA														
<212			phi1	a me	lano	gast	er									
<400	> 6	0														
atga			atca	gett	t											20
																20
<210	> 6	9														
<211:																
<212		AM			_											
<213:	> D:	roso	onı1.	a me	lano	gast	er									
<400																
cctga	aagc	et g	acat	tcca	t											20
<210																
<211>																
<212; <213;		IA.														
~~ £ 3 ?	· Di	USO	onila	a me.	lano	raste	er									

<400> actgca	70 gccg attcattaat g	2
<400>	71	
gaatta	atac gactcactat agggagatat catacacata cgatttag	48
<210> <211> <212> <213> <400> gaatta:	DNA Drosophila melanogaster	48
<210> <211> <212> <213>	21 DNA	
<400> tgtaaaa	73 acga cggccagtga a	21